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Rhei rhizoma and Glycyrrhiza uralensis mixture extracts protect esophageal mucosal damage in reflux esophagitis through the regulation of Nrf2 and NF-



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Purpose: The present study was designed to evaluate the anti-inflammatory, anti-oxidative stress activities, and differential regulation of Nrf2-mediated genes by Rhei rhizoma and Glycyrrhiza uralensis mixture extracts (RGE) and to determine the usefulness of antioxidants in the treatment of reflux esophagitis.

Methods: Reflux esophagitis was induced by ligation with a 2-0 silk thread both the pylorus and the transitional junction between the forestomach and the corpus, in Sprague-Dawley rats.

Results: Our results show that RGE administration markedly ameliorated mucosal damage upon histological evaluation. In serum, RGE significantly suppressed the oxidative stress biomarkers, such as reactive oxygen species (ROS), peroxynitrite (ONOO-), and thiobarbituric acid reactive substances (TBARS). The rats with reflux-induced esophagitis exhibited down-regulation of antioxidant-related proteins such as nuclear factor-erythroid 2-related factor 2 (Nrf2) and heme oxygenase-1 (HO-1) expression levels in the esophagus; however, the levels with treatment of RGE were significantly higher than those in vehicle-administrated and reflux-induced esophagitis rats. RGE treatment caused significant reductions in activation of NF- κ B transcription factor, especially the p65 subunit, in accordance with the significantly higher levels of inhibitory protein of NF- κ B expression. Thus, RGE significantly exhibited potent anti-inflammatory activities by suppressing the protein expression levels of pro-inflammatory proteins, COX-2 and iNOS, in the esophagus tissue.

Conclusion: Reflux esophagitis caused considerable levels of oxidative stress in the esophageal mucosa and the administration of RGE reduced the esophageal mucosa damage through the regulation of a potential cross-talks between Nrf2 and NF- κ B pathways. Our findings should be considered as supplementary therapy in the prevention or treatment of reflux esophagitis.

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The Banhabaekchulcheonma-tang, a traditional herbal formula, suppressed adipogenesis by PPAR- α pathway regulation



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Purpose: To confirm the anti-obesity effects of Banhabaekchulchunma-tang (BCT), we used the differentiated 3T3-L1 adipocytes.

Methods: The efficacy of anti-obesity on BCT was evaluated by differentiated 3T3-L1 cell line. After differentiation for 7 days, we detected the level of TG and klotho in supernatant by elisa. To confirm gene expression, we were performed by microarray.

Results: TG and klotho contents were reduced by approximately 73% and 72%, respectively, especially when the MDI-induced 3T3-L1 cell were suppressed using 100 μ g/mL BCT. We detected 250 differentially expressed genes in the experimental group. In 250 detected genes, we selected the 154 genes which recovery to control group. The gene expression related with lipid metabolism detected PPAR- α signaling pathway and validated genes; PPAR- α , ap2 and CEBP- α .

Conclusion: The results suggest that BCT has an efficacy that strongly limits adipogenesis through the inhibition of the PPAR- α signaling pathway.

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Genetic association of coding region polymorphism in PON1 with Dampness-phlegm pattern among Korean stroke patients



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Purpose: In this study, we elucidated association of polymorphisms, located at PON1 promoter and coding region, with dampness-phlegm pattern (DP) among Korean stroke subjects.

Methods: Pattern identification (PI) of subjects was diagnosed by two KOM special doctors and genotypes were performed by Snapshot method.

Results: Relation of PON1 polymorphisms on DP among small scale subjects, fifty eight in DP group and one hundred forty in non-DP group, showed that frequency of M allele in DP group was significant higher than non-DP group [OR=4.032 (95% CI, 1.595-10.204), $p=0.0032$], and subjects with M allele was also larger in DP group than non-DP group [OR=3.023 (95% CI, 1.512-10.701), $p=0.0032$]. To confirm the association of L55 M polymorphism with DP, we replicated the genetic association among large scale stroke subjects, three hundred nineteen in DP group and five hundred thirty five in non-DP group. The frequency of subjects with M allele was also higher in DP group than non-DP group [OR=1.704 (95% CI, 1.059-2.742), $p=0.028$].